Package ‘diffusr’

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Type Package

Title Network Diffusion Algorithms

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Description Implementation of network diffusion algorithms such as heat diffusion or Markov random walks. Network diffusion algorithms generally spread information in the form of node weights along the edges of a graph to other nodes. These weights can for example be interpreted as temperature, an initial amount of water, the activation of neurons in the brain, or the location of a random surfer in the internet. The information (node weights) is iteratively propagated to other nodes until an equilibrium state or stop criterion occurs.

URL https://github.com/dirmeier/diffusr

BugReports https://github.com/dirmeier/diffusr/issues

License GPL (>= 3)

Depends R (>= 3.4)

LazyData TRUE

LinkingTo Rcpp, RcppEigen

Imports Rcpp, igraph, methods

Suggests knitr, rmarkdown, testthat, lintr, Matrix

VignetteBuilder knitr

RoxygenNote 6.0.1

SystemRequirements C++11

NeedsCompilation yes

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Repository CRAN

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Description

Network diffusion algorithms in R.

Author(s)

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References


Koehler, S., Bauer, S., Horn, D., & Robinson, P. N. (2008), Walking the interactome for prioritization of candidate disease genes. *The American Journal of Human Genetics*


https://en.wikipedia.org/wiki/Laplacian_matrix
heat.diffusion

Graph diffusion using a heat diffusion process on a Laplacian matrix.

Description

An amount of starting heat gets distribution using the Laplacian matrix of a graph. Every iteration (or time interval) heat streams from the starting nodes into surrounding nodes.

Usage

heat.diffusion(h0, graph, t = 0.5, ...)

## S4 method for signature 'numeric,matrix'
heat.diffusion(h0, graph, t = 0.5, ...)

## S4 method for signature 'matrix,matrix'
heat.diffusion(h0, graph, t = 0.5, ...)

Arguments

- **h0**: an n x p-dimensional numeric non-negative vector/matrix of starting temperatures
- **graph**: an (n x n)-dimensional numeric non-negative adjacence matrix representing the graph
- **t**: time point when heat is measured
- **...**: additional parameters

Value

returns the heat on every node as numeric vector

References

https://en.wikipedia.org/wiki/Laplacian_matrix

Examples

# count of nodes
n <- 5
# starting distribution (has to sum to one)
h0 <- as.vector(rmultinom(1, 1, prob=rep(.2, n)))
# adjacency matrix (either normalized or not)
graph <- matrix(abs(rnorm(n*n)), n, n)
# computation of stationary distribution
ht <- heat.diffusion(h0, graph)
hub.correction

Correct for hubs in an adjacency matrix

Description
Correct for hubs in an adjacency matrix

Usage
hub.correction(obj)

Arguments
 obj matrix for which hubs are corrected

Value
returns the matrix with hub correction

Examples
W <- matrix(abs(rnorm(10000)), 100, 100)
cor.hub <- hub.correction(W)

nearest.neighbors

Graph diffusion using nearest neighbors

Description
For every node in a set of nodes the graph gets traversed along the node’s shortest paths to its neighbors. Nearest neighbors are added until a maximum depth of k is reached. For settings where there are more than k neighbors having the same distance, all neighbors are returned.

Usage
nearest.neighbors(nodes, graph, k = 1L, ...)

## S4 method for signature 'integer, matrix'
nearest.neighbors(nodes, graph, k = 1L, ...)

Arguments
 nodes a n-dimensional integer vector of node indexes (1-based) for which the algorithm is applied iteratively
 graph an (n x n)-dimensional numeric non-negative adjacency matrix representing the graph
 k the depth of the nearest neighbor search, e.g. the depth of the graph traversal
 ... additional parameters
Value

returns the kNN nodes as list of integer vectors of node indexes

Examples

```r
# count of nodes
n <- 10
# indexes (integer) of nodes for which neighbors should be searched
node.idxs <- c(1L, 5L)
# the adjacency matrix (does not need to be symmetric)
graph <- rbind(cbind(0, diag(n-1)), 0)
# compute the neighbors until depth 3
neighs <- nearest.neighbors(node.idxs, graph, 3)
```

normalize.laplacian  
_Calculate the Laplacian of a matrix_

Description

Calculate the Laplacian of a matrix

Usage

normalize.laplacian(obj, ...)

Arguments

obj  
matrix for which the Laplacian is calculated

...  
additional params

Value

returns the Laplacian

Examples

```r
W <- matrix(abs(rnorm(10000)), 100, 100)
lapl.W <- normalize.laplacian(W)
```
normalize.stochastic

*Create a stochastically normalized matrix/vector*

**Description**

Create a stochastically normalized matrix/vector

**Usage**

```r
normalize.stochastic(obj, ...)
```

**Arguments**

- `obj`: matrix/vector that is stochastically normalized
- `...`: additional params

**Value**

returns the normalized matrix/vector

**Examples**

```r
W <- matrix(abs(rnorm(10000)), 100, 100)
stoch.W <- normalize.stochastic(W)
```

random.walk

*Graph diffusion using a Markov random walk*

**Description**

A Markov Random Walk takes an initial distribution \( p_0 \) and calculates the stationary distribution of that. The diffusion process is regulated by a restart probability \( r \) which controls how often the MRW jumps back to the initial values.

**Usage**

```r
random.walk(p0, graph, r = 0.5, niter = 10000, thresh = 1e-04,
          do.analytical = FALSE, correct.for.hubs = FALSE)
```

```r
## S4 method for signature 'numeric, matrix'
random.walk(p0, graph, r = 0.5, niter = 10000,
          thresh = 1e-04, do.analytical = FALSE, correct.for.hubs = FALSE)
```

```r
## S4 method for signature 'matrix, matrix'
random.walk(p0, graph, r = 0.5, niter = 10000,
          thresh = 1e-04, do.analytical = FALSE, correct.for.hubs = FALSE)
```
random.walk

Arguments

p0 an n x p-dimensional numeric non-negative vector/matrix representing the starting distribution of the Markov chain (does not need to sum to one).

graph an (n x n)-dimensional numeric non-negative adjacency matrix representing the graph

r a scalar between (0, 1). restart probability if a Markov random walk with restart is desired

niter maximal number of iterations for computation of the Markov chain. If thresh is not reached, then niter is used as stop criterion.

thresh threshold for breaking the iterative computation of the stationary distribution. If the absolute difference of the distribution at time point t-1 and t is less than thresh, then the algorithm stops. If thresh is not reached before niter, then the algorithm stops as well.

do.analytical boolean if the stationary distribution shall be computed solving the analytical solution or rather iteratively

correct.for.hubs if TRUE multiplies a correction factor to the nodes, such that the random walk gets not biased to nodes with high degree. In that case the original input matrix will be normalized as:

\[ P(j|i) = \frac{1}{\text{degree}(i)} \times \min(1, \frac{\text{degree}(j)}{\text{degree}(j)}) \]

Note that this will not consider edge weights.

Value

returns a list with the following elements

• p.inf the stationary distribution as numeric vector

• transition.matrix the column normalized transition matrix used for the random walk

References


Koehler, S., Bauer, S., Horn, D., & Robinson, P. N. (2008), Walking the interactome for prioritization of candidate disease genes. The American Journal of Human Genetics

Examples

# count of nodes
n <- 5

# starting distribution (has to sum to one)
p0 <- as.vector(rmultinom(1, 1, prob=rep(0.2, n)))

# adjacency matrix (either normalized or not)
graph <- matrix(abs(rnorm(n*n)), n, n)
# computation of stationary distribution
pt <- random.walk(p0, graph)
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